CRF Errors Corrected by the STIC Systems Branch   1652

CRF Processing Date: 12/7/2000
Edited by: /A/
Verified by: /A/   (STIC staff

ENTERED

RECEIVED #9

DEC 21 2000

Serial Number: _09/492,029_

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☑ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: _Seq 2 - corrected <222> response_

_____

_____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/492,029

DATE: 12/18/2000
TIME: 15:05:02

Input Set : A:\Pto.amc
Output Set: N:\CRF3\12182000\I492029.raw

```
 3  <110> APPLICANT: Zuker, Charles S.
 4         Adler, Jon Elliot
 5         Lindemeier, Juergen
 6         The Regents of the University of California
 8  <120> TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell
 9         Specific G-Protein Beta Subunit
11  <130> FILE REFERENCE: 02307E-092710US
13  <140> CURRENT APPLICATION NUMBER: US 09/492,029
14  <141> CURRENT FILING DATE: 2000-01-26
16  <150> PRIOR APPLICATION NUMBER: US 60/117,404
17  <151> PRIOR FILING DATE: 1999-01-27
19  <160> NUMBER OF SEQ ID NOS: 5
21  <170> SOFTWARE: PatentIn Ver 2.1
23  <210> SEQ ID NO: 1
24  <211> LENGTH: 156
25  <212> TYPE: DNA
26  <213> ORGANISM: Rattus sp.
28  <220> FEATURE:
29  <223> OTHER INFORMATION: rat tongue circumvallate papillae taste receptor
30         cell cDNA clone 165-17
32  <400> SEQUENCE: 1
33  aacaaaaggg cataaagaaa gtggctggga gggagccagg atactaggag tgacacctat 60
34  agtcatgggc tgagcgctct ggccattccc argccggaca aaggctgctg gtagcccagg 120
35  agtcatctag ggtgggqagg gtctgttctt gtttat                            156
38  <210> SEQ ID NO: 2
39  <211> LENGTH: 1520
40  <212> TYPE: DNA
41  <213> ORGANISM: Rattus sp.
43  <220> FEATURE:
44  <221> NAME/KEY: CDS
45  <222> LOCATION: (78)..(1097)
46  <223> OTHER INFORMATION: rat taste cell specific G-protein beta 3 subunit
47         (TC-Gbeta3)
49  <400> SEQUENCE: 2
50  gggcgcctgg gaagcggaaa cctgggagaa atccagctag agcccaagag ccaggactac 60
52  cccttgacct gtgaacc atg ggg gag atg gag cag ctg aag cag gag gcg     110
53                   Met Gly Glu Met Glu Gln Leu Lys Gln Glu Ala
54                    1               5                  10
56  gag cag ctc aag aag cag att gct gat gcc agg aaa gcc tgt gcg gac   158
57  Glu Gln Leu Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp
58           15                  20                  25
60  atc act ctg gct gag ctt gtg tct ggc ctg gag gtg gtg gga cga gtc   206
61  Ile Thr Leu Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val
62           30                  35                  40
64  cag atg cgg aca cgg agg acg tta agg gga cac ctg gct aag atc tat   254
65  Gln Met Arg Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr
66       45                  50                  55
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Input Set : A:\Pto.amc
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                                                                 302
68 gcc atg cac tgg gcc act gac tct aag ctg cta gta agt gcc tcg cag
69 Ala Met His Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln
70  60                65                   70                75
                                                                 350
72 gat ggg aag ctg atc gtg tgg gac act tac acc acc aat aag gtg cat
73 Asp Gly Lys Leu Ile Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His
74            80                   85                   90
                                                                 398
76 gct atc ccg ctg cgt tcc tcc tgg gtc atg acc tgt gcc tat gca cca
77 Ala Ile Pro Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro
78            95                  100                  105
                                                                 446
80 tca ggg aac ttc gtg gca tgt ggg ggg cta gat aac atg tgc tca atc
81 Ser Gly Asn Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile
82       110                  115                  120
                                                                 494
84 tac agc ctc aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gaa ctc
85 Tyr Ser Leu Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu
86       125                  130                  135
                                                                 542
88 tcg gct cac aca ggt tat ctc tcc tgt tgc cgc ttc ctg gat gac aac
89 Ser Ala His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn
90 140                  145                  150                  155
                                                                 590
92 aac att gtg act agc tct ggg gac acc acg tgt gcc ttg tgg gac att
93 Asn Ile Val Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile
94            160                  165                  170
                                                                 638
96 gag acg ggg cag cag aag aca gtg ttc gtg gga cac act ggt gac tgc
97 Glu Thr Gly Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys
98       175                  180                  185
                                                                 686
100 atg agc ctg gct gtg tcc cca gac tac aaa ctc ttc atc tcg gga gct
101 Met Ser Leu Ala Val Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala
102       190                  195                  200
                                                                 734
104 tgt gat gcc agc gcc aag ctc tgg gat gtg agg gaa ggg acc tgt cgc
105 Cys Asp Ala Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg
106       205                  210                  215
                                                                 782
108 cag act ttc act ggc cac gag tca gac atc aat gct atc tgt ttc ttt
109 Gln Thr Phe Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe
110 220                  225                  230                  235
                                                                 830
112 ccc aat ggg gag gcc atc tgc act ggc tca gat gat gcc tcc tgc cgc
113 Pro Asn Gly Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg
114            240                  245                  250
                                                                 878
116 ctc ttt gac ctg agg gca gac cag gaa ctg aca gcc tac tcc cac gag
117 Leu Phe Asp Leu Arg Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu
118       255                  260                  265
                                                                 926
120 agc atc atc tgt ggc atc acg tcc gta gcc ttc tca ctc agt ggt cgc
121 Ser Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg
122       270                  275                  280
                                                                 974
124 ctg ctc ttt gct ggc tat gat gac ttc aac tgc aat gtc tgg gac tct
125 Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser
126       285                  290                  295
                                                                 1022
128 ctg aag tgt gag cgt gta ggc gtt ctt tct ggc cat gac aac aga gtc
129 Leu Lys Cys Glu Arg Val Gly Val Leu Ser Gly His Asp Asn Arg Val
130 300                  305                  310                  315
                                                                 1070
132 agt tgc ctg ggg gtc aca gct gac ggc atg gct gtg gcc act gga tcc
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133 Ser Cys Leu Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser
                         320                325                330
134                                                                        1117
136 tgg gac agc ttc ctc aag atc tgg aac tgaggaggct ggaggaagag
137 Trp Asp Ser Phe Leu Lys Ile Trp Asn
                    335                340
138                                                                        1177
140 gtgggaagcc atgaaggctc tcagctgact cctatgccct gtctccttag ggtcagtctt 1177
142 ctataccctg gggccactcc cagtaaactt ccttctaagt gcaggtggga ttataggagt 1237
144 gtgcctttgg gagtagcagg gtcacaaggg caaagaactg ccccattttcc tccagggcct 1297
146 ctcctctcca cagtcctcat agcttctccc ttcataaaca agaacagacc ctccccaccc 1357
148 tagatgactc ctgggctacc agcagcgttt gtccggcctg ggaatggcca gagcgctcag 1417
150 cccatgacta taggtgtcac tcctagtatc ctggctccct cccagcgact ttctttctgc 1477
152 ccttttgttc tctcttatta cctaataaaa tgtagcatcc tgg              1520
155 <210> SEQ ID NO: 3
156 <211> LENGTH: 340
157 <212> TYPE: PRT
158 <213> ORGANISM: Rattus sp.
160 <400> SEQUENCE: 3
161 Met Gly Glu Met Glu Gln Leu Lys Gln Glu Ala Glu Glu Leu Lys Lys
162  1                5                10                15
164 Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Ile Thr Leu Ala Glu
165                20                25                30
167 Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
168                35                40                45
170 Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
171        50                55                60
173 Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
174  65                70                75                80
176 Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
177                85                90                95
179 Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
180                100                105                110
182 Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Ser Leu Lys Ser
183        115                120                125
185 Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
186        130                135                140
188 Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
189 145                150                155                160
191 Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
192                165                170                175
194 Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
195                180                185                190
197 Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
198        195                200                205
200 Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
201        210                215                220
203 His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
204 225                230                235                240
206 Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
207                245                250                255
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12/18/00

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209 Ala Asp Gln Gln Leu Thr Ala Tyr Ser His Glu Ser Ile Ile Cys Gly
210            260                 265                 270
212 Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
213            275                 280                 285
215 Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Leu Lys Cys Glu Arg
216       290                 295                 300
218 Val Gly Val Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
219 305                 310                 315                 320
221 Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
222                 325                 330                 335
224 Lys Ile Trp Asn
225                 340

229 <210> SEQ ID NO: 4
230 <211> LENGTH: 1523
231 <212> TYPE: DNA
232 <213> ORGANISM: Homo sapiens
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (7)..(1029)
237 <223> OTHER INFORMATION: human taste cell specific G-protein beta 3 subunit

239 <400> SEQUENCE: 4
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241         Met Gly Glu Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu
242          1               5                  10
244 aag aag cag att gca gat gcc agg aaa gcc tgt gct gac gtt act ctg      96
245 Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu
246  15                  20                  25                  30
248 gca gag ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cgg     144
249 Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg
250                  35                  40                  45
252 acg cgg cgg acg tta agg gga cac ctg gcc aag att tac gcc atg cac     192
253 Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His
254          50                  55                  60
256 tgg gcc act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag     240
257 Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys
258  65                  70                  75
260 ctg atc gtg tgg gac agc tac acc acc aac aag gtg cac gcc atc cca     288
261 Leu Ile Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro
262  80                  85                  90
264 ctg cgc tcc tcc tgg gtc atg acc tgt gcc tat gcc cca tca ggg aac     336
265 Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn
266  95                 100                 105                 110
268 ttt gtg gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc     384
269 Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu
270                 115                 120                 125
272 aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac     432
273 Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His
274                 130                 135                 140
276 aca ggt tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg     480
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277 Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val
278        145                     150                     155         528
280 acc agc tcg ggg gac acc acg tgt gcc ttg tgg gac att gag act ggg
281 Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly
282        160                     165                     170         576
284 cag cag aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctg
285 Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu
286 175                     180                     185             190 624
288 gct gtg tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc
289 Ala Val Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala
290                     195                     200             205     672
292 agt gcc aag ctc tgg gat gtg cga gag ggg acc tgc cgt cag act ttc
293 Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe
294        210                     215                     220         720
296 act ggc cac gag tcg gac atc aac gcc atc tgt ttc ttc ccc aat gga
297 Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly
298        225                     230                     235         768
300 gag gcc atc tgc acg ggc tcg gat gac gct tcc tgc cgc ttg ttt gac
301 Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp
302        240                     245                     250         816
304 ctg cgg gca gac cag gag ctg atc tgc ttc tcc cac gag agc atc atc
305 Leu Arg Ala Asp Gln Glu Leu Ile Cys Phe Ser His Glu Ser Ile Ile
306 255                     260                     265             270 864
308 tgc ggc atc acg tcc gtg gcc ttc tcc ctc agt ggc cgc cta cta ttc
309 Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe
310                     275                     280             285     912
312 gct ggc tac gac gac ttc aac tgc aat gtc tgg gac tcc atg aag tct
313 Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Met Lys Ser
314        290                     295                     300         960
316 gag cgt gtg ggc atc ctc tct ggc cac gat aac agg gtg agc tgc ctg
317 Glu Arg Val Gly Ile Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu
318        305                     310                     315        1008
320 gga gtc aca gct gac ggg atg gct gtg gcc aca ggt tcc tgg gac agc
321 Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser
322        320                     325                     330        1056
324 ttc ctc aaa atc tgg aac tgaggaggct ggagaaaggg aagtggaagg
325 Phe Leu Lys Ile Trp Asn
326 335                     340
328 cagtgaacac actcagcagc cccctgcccg accccatctc attcaggtgt tctcttctat 1116
330 attccgggtg ccattcccac taagctttct cctttgaggg cagtggggag catgggactg 1176
332 tgcctttggg aggcagcatc agggacacag gggcaaagaa ctgcccatc tcctcccatg 1236
334 gccttccctc cccacagtcc tcacagcctc tcccttaatg agcaaggaca acctgcccct 1296
336 ccccagccct ttgcaggccc agcagacttg agtctgaggc cccaggccct aggattcctc 1356
338 ccccagagcc actacctttg tccaggcctg ggtggtatag ggcgtttggc cctgtgacta 1416
340 tggctctggc accactaggg tcctggcct cttcttattc atgctttctc cttttctac 1476
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345 <210> SEQ ID NO: 5
346 <211> LENGTH: 340
347 <212> TYPE: PRT
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12/18/00

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/492,029

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